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Harry 1778 March EAST Version: 1.61.

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ANSWER 1 OF 21 BIGSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 2000:439021 BIOSIS DOCUMENT NUMBER: FREV200000439021

TITLE: The junctional multidomain protein AF-6 is a binding

partner of the RaplA GTPase and associates with the actin

cytoskeletal regulator profilin.

AUTHOR(S): Boettner, Benjamin; Govek, Eve-Ellen; Cross, Justin; Van

Aelst, Linda (1)

CORFORATE SOURCE: (1) Told Spring Harbor Laboratories, 1 Bungtown Road, Cold

Spring Harbor, NY, 11724 USA

SOURCE: Proceedings of the National Academy of Sciences of the

United States of America, (August 1, 2000) Vol. 97, No. 16,

pp. 9064-9869. print.

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ittari Tanga e:

The Afec growthin is a multidimain protoin that contains two a tentual Ras-kinding demains within its M terminus. Because it this reature, Abechas been isolated in both - ***twet** - ***hybrid*** and pip memical appropries and is postulated to be A p tential RAs- * * treffe to r* t rigin. Herein, we show that it is specifically the first Ras-binding romain of AF-0 that registes this interaction and that the Faz-polated Equipment in the age date with this mother was entry than the of specific Hamp, Why, as a MHR and STE applies. Who is defined labor more rate of had in the Basis

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YRIGHT 2000 Bittsia CORMENT NUMBER: FREVIII (000242205 Retincto acid and its receptors repress the expression and transactivation runctions of Nur $^{\circ\circ}$. A possible mechanism for the inhibition of apoptosis by retinoic abid. Fang, Hyo-Jin; Song, Mi-Ryoung; Lee, Soc-Kyung; Shin, ATTHOREST: Fui-Chul; Chai, Youn-Hee; Kim, Se Jong; Lee, Jae Woon; Lee, Mi-03k *11 1) Department of Microbiology, Institute for immunology JUREURAIE SOURCE: and Immunological Diseases, Yonsei University College of Medicine, Secul, 126-752 South Korea Experimental Cell Research, (May 1, 2000) Vol. 256, No. 2, WIRTE: pp. 545-764. ISSN: 0014-4827. DOCUMENT TYPE: Art.ble l'ANGUAGE: English CUMMARY LANGUAGE: Eng.ish AB NurV7 (NGFI-B) is an orphan nuclear receptor that has been implicated in activation-induced T-cell apoptosis. Retinoids, potent immune ***modulators*** , were shown to inhibit the activation-induced apoptosis of immature thymocytes and T-cell hybridomas. To illustrate the mechanism of the inhibition, we examined the effects of retinoic acid (RA) on the expression and transact vation functions of Nur?? in the human peripheral blood menonumiear cells and the human T-cel! loukemia, Jurkat. All-trans-RA remarkably repressed the DNA binding and transcriptional induction of Nur77. Among the two potential trans-acting factors that activate Nur77 gene promoter, i.e., AP-1 and related serum response factor (RSRF), all-trans-FA repressed DNA binding and reporter gene activity of AP-1 but not that cf RSRF, suggesting that the inhibition may be mediated through AP-1. We also demonstrated a posttranscriptional regulation of Nur77 function by retinoid receptors by showing that transactivation activity of $\operatorname{Mur} 7^{\frac{1}{2}}$ was significantly inhibited by cotransfection of RAKalpha or RMRalpha. Nur"7 bound RARalpha or RMRalpha in both yeast and mammalian. ****we** - ***hybrid*** tests, suggesting that direct ***protein*** - ***interaction*** between these receptors may mediate the inhibition. Taken all together, we demonstrated that RA repressed Nur77 function through multiple mechanisms that may provide the basis for RA inhibition on the apoptosis of activated T-lymphosytes. AMSWER 3 OF 31 BIOSIS COPYRIGHT 2000 BIOSIS ACTESSION IMMBER: 1999:496666 BIOSIS CHOUMEDT NUMBER: FREU1999 12496666 PITLE: The Borgs, a new family of Cdu42 and TC10 GTPase-interacting proteins. Toberty, Perara II; Ferlynsser, Bishani R.; Masara, Lan G. -1. Hell, University of Virginia och. I of Medicine, E ee Ulti Hespital West, Tharlottesmille, VA, ... We usw Ulti Hespital West, Tharlottesmille, VA, ... We usw THE BACK AS THIS: * * * * * * * * $139333 \cdot 10^{-10} \cdot 10^{-10} \cdot 10^{-10}$ -TREAT THE Antisle LANGUAGE: English JUMMARY JANGJAGE: English The bulliability of STPases plays key to les in the remnation of bell rotality as though mension they also retain to the kinds consequent, The first of the second of the

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HAT -target brist protein was mostly by solir when expressed on proteiny in MiH 202 deals, with sea accumulation in pentrane runf.

of Rho function and was reversed by overexpression of Rho. Surprisingly, it was independent of the ability to bind Cir42. Bord3 also inhibited in Alhase activity by a mechanism that was independent of Cdc42 binding. Harm rice expression rauses substantial delays in the spreading of hells in through a surfaces after replating, and the spread cells lacked stress tiles. We propose that the Bord proteins function as negative reducators of Rho STFase signaling.

L. ANEWER 4 OF 21 BIOSIS COPYRIGHT 2000 BROSIS

ACCESSION NUMBER: 1999:488133 BIOSIS DOCUMENT NUMBER: PREV199900488133

TITIF: Two distinct mutations of the RET receptor causing

hirschsprung's disease impair the binding of signalling '*'effectors''' to a multifunctional dooking site.

Ceneste, Olivier; Bidaud, Christelle; De Vita, Gabriella; Hofstra, Robert M. W.; Tartare-Deckert, Sophie; Buys,

Charles H. C. M.; Lencir, Gilbert M.; Santoro, Massimo;

Eillaud, Marc (1)

CORFORATE SOURCE: (1) Laboratoire de Genetique, CNRS UMR5641, 8 avenue

Rockefeller, 69373, Lyon Cedex 08 France

IMPROE: Human Molecular Genetics, (Oct., 1999) Vol. 8, No. 11, pp.

1989-1999.

ISSN: 0964-6906.

COCUMENT TYPE: Article LANGUAGE: English SUMMARY LANGUAGE: English

ATTH BULY:

The RET gene codes for a transmembrane tyrosine kinase which is a subunit of a multimeric complex that acts as a receptor for four structurally related molecules: the glial cell line-derived neurotrophic factor (GDNF), neurturin, artemin and persephin. Germline mutations of RET cause a dominantly innerited dysgenesis of the enteric nervous system known as Hirschsprung's disease (HSCR; aganglionosis megacolon). The majority of HSCR mutations results either in a reduction of desage of the RET protein or in the loss of RET function. Two novel distinct mutations of RET that led either to the deletion of codon 1059 (denoted DELIA1059) or to the substitution of a Pro for Leul06! have been identified in five HSCR families. In one large pedigree, two children born from asymptomatic consanguineous parents presented a severe form of HSCR and were found to carry the mutation at codon 1061 in the homonygous state. A tyrosine residue at position 1062 is an intracytoplasmic docking site that enables RET to recruit several signalling molecules, including the Shc adaptor protein. We now report that both HSCR mutations impair the fixation of Sho to RET and consequently prevent its phosphorylation. In addition, to RET and consequently prevent its phosphorylation. In addition, quantitative analysis in PC12 cells reveals that mutation DELTA1059 in a tovater the ability of EFT to transdrive a light rear simulational whoreas to at a light only partially immility the cimulation of EFT. Finally, we have a conducted that there exists are partly realist invia the disruption of the EFT. So interaction, a light way, there results are not rate that the citizens of transaction of transaction of the results of the conduction of the results of the conduction of the c bischemical explanation for the phenotype of patients carrying a homboygous mutation at coden 1061. Finally, these data indicate that YIAG is a multifunctional docking site that confers to RET the capacity to this be investigant sinualling pathways which exert a propial role during estate business and measurable.

LANGUAGE: English

receptors through irmution of trinclecular complexes, composed of a ligand, a receptor, and a negaran sultate oligosaccharide, all of which are members of particularly large families capable of multiple interactions in a cirklinatorial fashion. Understanding this large network of interactions in a cirklinatorial fashion. Understanding this large network of interactions in the case of the control of the case Taparity It must classical techniques routinely used to study ligand receptor interactions. We have used the yeast antiquest arthur the study of the in the FMF family. Both ligand and receptor estedomains are properly it dea and functional in the yeast. Busic FGF (bFGF) expressed in the yeast dimerizes spontaneously. This self-assembly occurs at low atfinity, which can be greatly enhanced by the introduction of heparin, supporting a defined role for heparin in bFGF dimeridation. Screening a rat embryo NWW. library with bFGF in the yeast ***two*** ***hybrid*** system identified a short variant of FGF receptor 1, found most frequently in embryonal and tumor cells and which possesses affinity toward bFGF that is significantly greater than that of the more abundant, full-length reseptor. We find the yeast ***two*** ***hybrid*** system, a most suitable alternative method for the analysis of growth factor-receptor interactions as well as for screening for novel interacting proteins and ** modulators * . of FGF and its receptors.

Lb ANSWER 6 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1999:255910 BIOSIS
DOCUMENT NUMBER: PREV199900255910

TITLE: The ubiquitin-homology protein, DAP-1, associates with

tumor necrosis factor receptor (p60) death domain and

induces apoptosis.

ANTHOR'S: Lieu, Mei-Ling; Lieu, Hsieu-Chi (1)

CORPORATE SOURCE: (1) Division of Immunology, Department of Medicine,

Graduate School of Medical Sciences, Cornell University

Medical College, New York, NY, 10021 USA

SOURCE: Journal of Biological Chemistry, (April 9, 1999) Vol. 274,

Nc. 15, pp. 10145-10153.

ISSN: 0021-9258.

DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

The tumor necrosis factor receptor, p60 (TNF-RI), transduces death signals via the association of its cytoplasmic domain with several intracellular proteins. By screening a mammalian cDNA library using the yeast '**two*** - ***hybrid*** clening technique, we isolated a ubiquitin-homology protein, DAP-1, which specifically interacts with the tytoplasmic death domain of TNF-RI. Sequence analysis reveals that DAP-1 chars of this person from any with the yeast CNT protein that is exactle in the californians of distributes to interact the interaction of the protein that is seen to be a set of the californians of distributes the first form of the first of the californians. The limit of the californians of the californians

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demain al prinser transcription factor. Tamiel, Det M., Boyn lie, Albert B. ATTHER : WAR HAIR SOURCE: il Department of Sell Biology, Vanderbilt Universit BUILDE: Molecular and Cellular Biology, May, 1999: Vol. 19, No. 1, pp. 3€14-3623. ISSN: 0100-7306. TIME: Article ANTATÉ: English NUMBER LANGUAGE: English plufeth is an Armadille repeat demain protein with structural similarity time cell adhesion octactors beta-catenin and plakoglobin. All threeproveins interact directly with the sytoplasmic domain of the ransmembrane sel. adhesion mole ule E-sadherin; beta-satenin and plakinglishin bind a carboxy-terminal region in a mutually exclusive manner, while pi20 binds the juxtamembrane region. Unlike beta-catenin and plakeglobin, place does not interact with alpha-catenin, the tumor suppressor adenomatous polyposis coli (APC), or the transcription factor Lef-1, suggesting that it has unique binding partners and plays a distinct role in the cadherin-catenin complex. Using p120 as bait, we conducted a yeast ***twp*** - ***nybrid*** screen and identified a nove! transcription factor which we named Kaiso. Kaiso's deduced amino acid sequence revealed an amino-terminal BTB/FOZ ***protein*** -***protein*** ***interaction*** domain and three darboxy-terminal mine fingers of the C2H2 DNA-binding type. Kaiso thus belongs to a rapidly growing family of PCZ-ZF transcription factors that include the Drosophila developmental regulators Tramtrak and Bric a brac, and the numan oncoproteins BCL-6 and PL3F, which are causally linked to non-Hodgkins' lymphoma and acute promyelocytic leukemia, respectively. Monoclonal antibodies to Kalso were generated and used to immunologalize the protein and confirm the specificity of the pl20-Kaiso interaction in mammalian cells. Kaiso specifically coprecipitated with a variety of pl20-specific monoclonal antirodies but not with antibodies to alpha- or beta-catenin, F-cadherin, or APC. Like other POZ-ZF proteins, Kaiso localized to the nucleus and was associated with specific nuclear dots. Yeast - ***hybrid*** interaction assays mapped the binding domains to Arm repeats 1 to 1 of p120 and the carbomy-terminal 200 amino acids of Kaiso. In addition, Haiso homodimerized via its POZ domain but it did not heterodimerize with BCL-6, which heterodimerizes with PLZF. The involvement of POZ-ZF proteins in development and cancer makes Kaiso an interesting candidate for a downstream ***effector*** of cadherin and/or p120 signaling. ANSWER 8 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS ACCESSION NUMBER: 1999:247872 BIOSIS DOCUMENT NUMBER: PREV199900247872 TITLE: Senes for calcineurin B-like proteins in Arabidopsis are differentially regulated by stress signals. He G Kumila, Tren, Šu, "Lamo, Harter, Klaus, Gruisser, Wilhele, luan, Sheng (1 i bepartredt it flant ana Min Blai Birlony, this asing THE BATE OF THE od Skild kiels, klakisky, w, kiel owe It wedink of the Mail has been by filthey yet in the Whitea States of America, April 1-, 1999 (7-1, 9, 17.), pp. 4718-4725. ISSN: 3737-84.4. TOWNS TYPE: Artible A11 11 74 48 : F. 11 31. TOWART LANGESTAR: Fi. Hinni. introduced and the contract of Marian Albania and Albania

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In contrast, AtCBL2 and AtCBL3 are scriptificatively empressed under all scriptions investigated. Our data suggest that AtCBL1 may act as a resular by subunit of a plant calcinvurineline activity mediating calcum simaling when tertain stress on Utiths.

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Charasterication of two subunits of Arabidopsis 198

proteasome regulatory complex and its possible interaction

with the CIPP complex.

ATTEOR S: Kwck, Shing F.; Staub, Jeffrey M.; Deng, Wing-Wang (1)

'OKPORATE SOUKCE: (1) Dep. Mol. Cell. Dov. Biol., Yale Univ., New Haven, CT

06520-8104 USA

JONES E. Journal of Molecular Biology, (Jan. 8, 1999) Vol. 285, No.

1, pp. 85-35. #88N: 0022-2x36.

DOCUMENT TYPE: Article LANGUAGE: English

The nuclear localized, multi-subunit COP9 complex (or COP9 signalosome) is a key developmental ***modulator*** involved in repression of photomorphogenesis. In an affort to further define the molecular actions of the COF9 complex, a yeast ***two*** ***hybrid*** interactive screen was undertaken to identify proteins that could directly interact with one subunit of this complex, namely FUSE/COPIL. This screen identified one specific interactive protein, AtS9, that is likely the Arabidopsis non-ATPase S9 (subunit 9) of the 19S regulatory complex from the 26S proteasome. AtS9 specifically interacts with FUS6/COP11 via the C-terminal domain of FUS6, COP11, which is distinct from the N-terminal domain necessary for FUS6 COP11 to interact with itself. As anticipated, AtS9 is not a member of the COP9 complex, but tightly associates with an ATPase subunit of the Arabidopsis 19S proteasome regulatory complex, AtS6A. Since all three proteins, FUS6/COP11, AtS9, and AtS6A, are present as complexed forms in vivo, the observed interaction implies that the COP9 complex may directly interact with the 19S regulatory complex of the 26S proteasome or other potential AtS9-containing complex. This notion is consistent with the parallel tissue-specific expression patterns and the similar, predominantly nuclear localization of both the COP9 complex and the AtS9 protein.

ANSWER 10 OF 21 BIOSIS COPYRIGHT 2000 PICSIS

ACCESSION NUMBER: 1999:17905 Biosin DOCUMENT NUMBER: PREV199900017905

Gene activation by the AraC protein can be inhibited by DNA looping between AraC and a look represent that interacts with AraC Function applications as a strong of the st TITE:

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NURT: Molecular Microbiology, (Nov., 1994) Vol. 50, No. 3, pr.

615-624.

188N: 1940-34 M.

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Thus, we have complined the functions of three detines or proper had achieve a new mode of gene equation by coping, in which the activator protein is an essential duration by 1104 regressor complex. The flexibility of the DNA log may facilitate this novel combinatorial arrangement of those proteins on the DNA. The requirement for protein Interactions between the Arad and LexA hybrids : :: gene regulation suggests that this regulatory circuit may prove useful as an E. coli-based ***two*** - ***hybrid*** | system. AMOWER 11 OF 21 PIOSIS COPYRIGHT 2005 PROSIS ACTERSION NUMBER: 1994:446725 BIOSIS

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Twing genetic means to dissert homotopius and heter lad us "" tripreteint" - ""preteint" tripreteinten :

FKR, the interieron-induced projein kinase.

AUTHOR [3]: Tan, Seng-Lai; Kathe, Michael G. (1)

WRFORATE BOURCE: (1) Dep. Microbiol., Sch. Med., Box 357242, Univ.

Washington, Seattle, WA 9×195 HSA

MARCE: Methods (Orlando), (July, 1998) Vol. 15, No. 3, pp.

207-223.

ISSN: 1046-2023.

DOG WENT TYPE: General Review LANGUAGE:

English The interferen-induced protein kinase, PKR, is a pivotal component of

interferon (IFN)-induced cellular antiviral and antiproliferative response. The identification and characterization of proteins, of both viral and cellular origins, that interact with PKR have proven to be a valuable probe for unraveling the cellular regulation and function of PKR. Several studies have demonstrated that PKR forms dimers and that dimerization is likely to be required for activation and/or catalytic function. It is therefore important to elucidate the mechanism of PKR

dimer formation and the role of FKR ***effectors*** in modulating kinase dimerization. Herein we describe the use of the two genetic approaches, the lambda repressor fusion and the yeast ***two*** -***hybrid*** systems, to detect and analyze homo- and heterotypic interactions with PKR. We also describe several biochemical methodologies commonly used in our laboratory to validate the genetic results. Although

the examples in this article focus on PKR, the techniques can easily be adapted to investigate protein-protein associations in a variety of experimenta: systems. Finally, given the important role of PKR as a mediator of IFN-induced antiviral and antiproliferative effects, these studies may provide clues to the development of reagents that target PKR

to enhance the therapeutic use of IFN in the treatment of disease.

L8 ANSWER 12 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS

AGGESSION NUMBER: 1998:236123 BIOSIS PRETT 43400236123

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system and in an in vitra interaction assay. Writhern blor revealed one major transport of about a khothat was prese protein digrated in sedium dedecy: sulfate-polyacrylamide gel electropic resis with an apparent notegular mass of of RDa. SET could be decembed in rath the nucleus and the cytoriasm of rat relis, as determined ry indirect laminifluorescence analysis and Western platting of fractionated cellular extracts with an affinity-purified antiserum raised against resembinant SGT (ACL.1). In H-1 virus-inferred rat and human sells, sumpared to mock-infersed controls, differences in the migration of SHI E lysestides were repealed after Western bl t analysis of total sellular extrasts. Moreover, the transient expression of MS proteins was sufficient to induce SUT modification. These results show that cellular SGT, which we have identified as an ASI-interacting protein, is modified by parvovirus intection as well as NS expression.

ANSWER 13 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1998:222407 BIOSIS COMMENT NUMBER: PREV1 39800222407

111111 Identification of the binding partners for flightless I, a

novel protein bridging the laugine-rich repeat and the

geisolin superfamilies.

AUTHOR(S):

Liu, Yu-Tsueng; Yin, Helen L. (1) (1) Dep. Ehyslol., Univ. Temas Southwestern Med. Cent., TORFORATE BOURCE:

Dallas, TX 75235 USA

SOURCE: Journal of Biological Chemistry, (April 3, 1998) Vol. 273,

No. 14, pp. 7920-7927.

ISSN: 0021-9258.

DOCUMENT TYPE: Article IANGUAGE: English

Flightless-! %flií) is a novel member of the gelsolin family that is important for actin organization during Drosophila embryogenesis and myogenesis. Drosophila fliI and the human homolog FLI both contain the classic gelsolin 6-fold segmental repeats and an amino-terminal extension of 16 tandem leucine-rich repeats (LRR). LRR repeats form amphipathic

interactions . Although there are close to 100 known LRR domain-containing proteins, only a few binding pairs have been identified. In this paper, we used biochemical and genetic approaches to identify proteins that interact with human FLI. In vitro synthesized FLI bound to and in-Sepharose and binding was reduced by competition with excess soluble actin. Actin binding was mediated through the gelsolin-like domain and not the LRR domain. Although the FLI LPR module is most closely related to the LRR domains of Ras-interactive projeins, FLI does not associate with Pas, selected Ras ***effectors*** , or other Ras-related small GTPases.

-**Two*** - ***bybrid*** screens using FET LRR as bait identified a nevel IRF finding partner. The 2.65-kilchase pair (kb) clone from the content some sail to a still have a man of explanation of the content some sail to be a separate, as a subject of the content some sail to be a separate, as a subject of the sail to be a separate.

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rripper latte - represente - trinterationett an Aggetia. to religion mechanisms at all levels in rividually responsive systems. These interactions occur excrapeliularly and include ligand-receptor interactions, sell adhesion, antigen recognition, and virus-host recognition. Intracellular of typicality - occupients.

"" finterartions " " o wur in the formation of multi-protein fumplemes, during the assembly he sytoskeletal elements, and between reseptor-* the Hesteritt , as well as the Hesteritt - * the Hesteritt , note pulses it signal transduction pathways. Finally, assembly of

tranship linal machinery involves protein interactions. The yeast

... two... - ... hytrid*. * method is a rowerful technique for analyzing these ***protein*** - ***protein*** ***!nteractions*** . Sin e the publication of this technique in the late 1980s, the robust nature and :ar-reaching utility of yeast '**two*** - ***hybrid*** systems for functional expression library cloning has led to the identification of many novel proteins in all areas of biological life science research. Additionally, ***two*** - ***hybrid*** techniques provide a rapid and versatile system for the further tharacterization of discrete

protein - ***protein*** ***!n.eractions*** . Recent variations on the basic system have enabled application well beyond protein pairs, to investigate multi-protein complexes and protein-nucleotide interactions. Yeast ****wo*** - ***bybrid*** methods necessitate expression and subsequent interaction between a "protein of interest" functional pair within the yeast cell, ultimately driving reporter gene expression and thus effectively linking

yeast cell phenotype. Functional ***protein*** - ***protein***

interactions using the ***twe*** - ***hybrid*** techniques have been demonstrated for all levels of cellular biology; however, until resently, extrahellular - ***protein*** - ***protein**

interactions were excluded from investigations using this technique. Investigations from several labs have now demonstrated that extracellular proteins can be studied using ***two*** - ***hybrid*** methods, thereby enabling intense study of extracellular protein partners using the robust nature and the genetic power of yeast.

ANSWER 15 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS

1998:71512 BIOSIS FREV1995UCTUBLA ACCESSION NUMBER: COCUMENT NUMBER:

Symponin, a FDZ protein that blads symbolar symplasmic

icalis.

St. S. Taner, C. Man. P., Pinnser ann. Factales, Rockmans, Butters, Physics, Act, Louise Ct., Nucl. Phys. B 2011 (1997) 1 and p. Phys. ATTER :

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TEGELM NUMBER: FREU194677731369 C TOMENT NUMBER:

Discrimination of amine acids mediating ras kinding from mominteracting residues affecting Rat artivation by double

nutant analysis.

Jaitner, Birgit K.; Becker, Joerg; Linnemann, Thomas; ATTEGE :

Herrmann, Christian; Wittinghofer, Altred; Block, Christoph

(1) Fortfach 10 28 64, D-44006 Dortmand Germany PRESERVE SOURCE:

Journal of Piological Chemistry, News. 71, 1990s Vol. 177, SOURCE:

No. 40, pp. 29476-14943.

188N: 0021-925%.

Article LANGUAGE: English.

The contribution of residues outside the Was binding domain of Raf. RafRBC) ty Ras-Raf interaction and Ras-dependent Ra: activation has remained unresolved. Here, we utilize a double mutant approach to identify complementary interacting amino acids that are involved in Ras-Raf interaction and activation. Biochemical analysis demonstrates that Naf-Arg39 and Raf-Arg67 from RafRBD are interacting residues complementary to Ras-Glu37 located in the Ras - ***effector** region. Raf-Arg59 and Raf-Argov also mediate interaction with Ras-Glu3? in Ras-dependent Raf activation. The characteristics observed here can be used as criteria for a role of residues from other regions of Raf in Ras-Raf interaction and activation. We developed a quantitative ***two*** - ***hybrid*** system as a tool to investigate the effect of point mutations on

protein - ***protein*** ***interactions*** that elude biochemical analysis of bacterially expressed proteins. This assay shows that Raf-Ser257 in the RafCR2 domain does not contribute to Ras-Raf interaction and that the Raf-S237L mutation does not restore Raf binding to Ras-E37G. Yet, Raf-S217L displays high constitutive kinase activity and further activation by Ras-G12V/E3°G is still impaired as compared with activation by Ras-G12V. This strongly suggests that the RafCR2 domain is an independent demain involved in the control of Raf activity and a common mechanism for constitutively activating mutants may be the interference

with the inactive ground state of the kinase.

ANSWER 17 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1997:314190 BIOSIS POSTMENT NUMBER: PREV199799604678

Modulator protein RsbR regulates environmental TITLE:

signalling in the general stress pathway of Bacillus

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Akhar, Samina; Kama, Chama Min; Nelsenko, Tatiana A.; ATTH Egg::

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Molecular Microbiology, Class Vol. 24, No. 3, 43, Defect

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erfacts in empression of para-B-dependent reporter fusion and in combination with the errsb mutations. To determine interaction of RshR with other Rsb proteins.

With ability of with type or notant back to a divate transdription in the yeast that the continuous with other Bai regulators. In the pasis of this menetic analysis, we obvious that bais is a positive regulator which modulates signath activity in response to salt and heat stress. Our data further suggest that: [1] Rsky influences the anticonist runction of RSES by direct triprotein.
trip reduct tringer and but ; and it this interaction with.

ksp3 is likely controlled by the phosphorylation state of RSES.

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्रक्तिः । अस्य ३५ स्टा<u>ल</u> A MESSION NUMBER: FRETT9419949943142 LOCUMENT NUMBER:

Modulation of the Escherichia ogli sigma-E (RycE) TITLE:

Heat-shock transcription-factor activity by the RseA, Renk

and RseC proteins.

Missiakas, Dominique; Mayer, Matthias P.; Lemaire, Marc; AUTHOR (5):

Georgopoulos, Costa; Raina, Satish (1)

CORFORATE SOURCE: (1) Dep. Biochimie Med., Centre Med. Univ., 1 rue

Michel-Servet, 1211 Geneve 4 Switzerland

Malegular Microbiology, (1997) Vol. 24, No. 2, pp. 355-371. POURCE:

ISBN: 0080-382M.

DOCUMENT TYPE: Article LANGUAGE: Enalish

AB The sigma-E (RpoE) transcription factor of Escherichia coli regulates the expression of genes whose products are devoted to extracytoplasmic activities. The sigma-E regulor is induced upon misfolding of proteins in the periplasm or the cater membrane. Similar to other alternative sigma factors, the activity of sigma-E is tightly regulated in E. coli. We have previously shown that sigma-E is positively autoregulated at the transcriptional level. DNA sequencing, coupled with transcriptional analyses, have shown that sigma-E is encoded by the first gene of a four-dene operon. The second gene of this operon, rseA, encodes an anti-sigma-E activity. This was demonstrated at both the genetic and biochemical levels. For example, mutations in rseA constitutively increase sigma-E activity. Consistent with this overproduction of RseA leads to an inhibitory effect on sigma-E activity. Topological analysis of RseA sudgests the existence of one transmembrane domain, with the N-terminal part localized in the cytoplasm. Overproduction of this N-terminal domain alone was shown to inhibit sigma-E activity. These observations were confirmed in vitro, because either purified RseA or only its purified N-terminal demain inhibited transpription from E-sigma-E-dependent promotors. Furthermore, EseA and sigma-E to-purify, and can be co-immunoprecipitated, and chemically cross-linked. The sigma-E activity is further regulated by the products of the remaining genes in this gramming in the last of the efficiency of the property control of the first terms of the per up a company of the company of t

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Bow wamlings in the Letter Letter to the LEE of False of LYM on a VAR which then the and 199-1 receptors in the continuous

factor-1 [IGF-1] type 1 reptor [IGF-1K* has been reported in some solder Interaction of St and GAF with Ik and IGF-1k was e-investible in the ***two** - nyprio system in big34 activation in S. Gerevisiae. The experiments were performed with the cytoplasmic beta dimain of IR and ISF-IR and various SH2-subdomains it CYI and GAF. Mone of the subdomains of SYF and GAF tested were able to a mirrate his? last, whereas these reporter genes were strongly a mirrated when jet was used as we have resently shown. Thus, interaction of SYP and GAF with IR and IGF-IR, if any, would be weak and/or transient as compared to that of pab.

ANSWER IN OF 21 BIOSIS COLYRIGHT 2000 FIRSTS

ATTERSION NUMBER: 1995:528173 BIOSIS : Company North : PPETTIGHT GREAT 473

Interaction of the protein nucleasindin with 3-aid, as

revealed by the yeast ***towerr - ***hybrig***

system.

Mochizuki, Nacki; Hibi, Masahiko; Kanai, Yoshiyuki; Insel, AUTHOR(S):

Paul A. (1)

(1) Dep. Fharmacol., Univ. California San Diego, 9500 TORKORATE SOURCE:

Gilman Drive, La Jolla, CA 92093-003€ USA

FERS Letters, (1995) Vol. 373, No. 2, pp. 155-158. : TOURCE:

ISSN: 0014-5793.

CATCHENT TYPE: Article LANGUAGE: English

AB The heterotrimeric G protein, G-alpha-i2, transduces signals from seven membrane spanning receptors to ***effectors*** such as adenylyl cyclase and ion channels. The purpose of this study was to identify these or other dellular proteins that interact with G-alpha-i2 by use of the yeast ***two*** - ***hybrid*** system. A human 3 cell cDNA library was screened by this system using full length G-alpha-i2. Four positive colonies were obtained. Two of the four were identified as nucleobindin, a caldium binding protein and a putative antigen to which anti-nuclear antibodies are generated in mide with a disorder that resembles systemic lupus erythematosus. Nucleobindin has a leucine zipper, EF hands, and a signal peptide sequence and is thought to localize to the hubleus as well as being secreted. The specificity of interaction between G-alpha-i2 and nucleobindin was confirmed by an in vitro binding assay using recombinant proteins. Transfection of G-alpha-i2 and nucleobindin in COS cells increased G-alpha-il expression relative to cells transfected with G-alpha-i2 and mock vector. Our results indicate that the yeast - ***two*** - ***hybrid*** system provides a means to identify novel proceins that interact with G-alpha proteins. Nucleobindin appears to

represent one of those proteins.

ANSWER 21 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS

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Plitari, Stephine; Yi, Sinayin; Flumer, Wardill 1.;

Hausladen, Denek; Ish wy, Minnayl W.; Inherly, istrate.

A.; Shaw, Andrew S. . 1.

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of per and was mediated by bot he SH3 and in tyrosing phosphorylation of per and was mediated by both the SH condition of p59-fvn. To phosphorylation of p61 by p59-fvn. requirements SH3 domain, demonstrating that one runction kinase SH3 domains is to bind and present Jertain substrates to the kinase. As pt2 contains at least live SH3-domain-binding motifs and multiple tyrosine phosphorylation sites, pol may interact with other signalling melecules via SH3 and SH2 domain interactions. Here we show that the SHR and/or SHR domains of the signalling proteins $\operatorname{Grb2}$ and prosping it ase "-damma-l can interact with real both in vitro and in vivo. Thus, we propose that one function of the tandemly occurring SH3 and SHZ domains of src family kinases is to bind p62, a multifunctional SH3 and SH2 domain adapter protein, linking src family kinases to downstream ***effector*** and regulatory molecules.

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AMSWEB 1 OF 4 BIOSIS COPYRIGHT III. BIOSIS

Tyrosine sultation: A fitmodulatorith of extracellular fiftenessions of extracellular fittenessions. TYSSION NUMBER: 2000:226020 BIOSIS FREVIOR 10022691 PARAMETER STREET Tyr sine sulfation: A - ***modulator*** of extrameliular Keng, John W.; Bertonni, Carolyn S. 91-ATTHON 81: I) Department of Molecular and Tell E. 1849, University of California, Berkeley, CA, 98 ps USA TORICHATE SOMECE: Themistry & Billow Jordan , Marth, 1877 W. J. W. J. SUMBOR: co. R57-R61. 188M: 1774-6521. IN TIMENT TYPE: Article LANGUAGE: English SUMMARY LANGUAGE: English => i kwic ipin tot L10 ANSWER 1 OF 4 BIOSIS COPYRIGHT 2000 BIOSIS Tyrosine sulfation: A ***modulator*** of extracellular ***protein*** - ***protein*** ***interactions*** . ACCESSION NUMBER: 2000:226020 BIOSIS DOCUMENT NUMBER: PREV200000226020 Tyrosine sulfation: A ***modulator*** of extracellular TITLE: ***protein*** - ***protein*** ***interactions*** . Kehoe, John W.; Bertozzi, Carolyn R. (1) AVIHOR SI: (1) Department of Molecular and Cell Biology, University of CORPORATE SOURCE: Cal fornia, Berkeley, CA, 94720 USA Chemistry & Biology (London), (March, 2006) Vol. 7, No. 3, COMBOR. pp. REV-R61. ISSN: 1074-5521. DOCUMENT TYPE: Article LANGUAGE: English STAMARY LANGUAGE: English 110 AMSWER 7 OF 4 BIOSIS COPYRIGHT 2000 PIQSIS . . the ras signaling pathway, i.e., it downrequiates activated ras via its catalytic demain, and it also participates in the downstream signaling pathway by mediating ***protein*** ***effector*** ***protein*** ***interaction*** . Missense mutations presumably leading to ras Wil activation were previously detected in this some, in a surset if holds. I haddese. . . enelin britisee: Ine:18291. Birdis Empression of randiane artifacting protect in taken the Martin has to the call. Parchard, Inle; Millers, Inle; Lancard, Ben; Barra, Acot; Schiby, Sinctio: Esp Livie, Cart, Leviev, Amor, Pricinal, El+an (1) i Suranne levy ne acherlus luhu, Inst. Besetu, Chair John Blod. Surt., leu-Hachuret Sevel lythe THE BATE OF THE Working Earlies By, During Live Co. Mr. Woods His

Signatura de la composición del composición de la composición de la composición del composición de la composición de la

MAILY NOVEL TRANSPETETE NO DOME N, FRANTO B, SHIN M K, BALSTO Mar was to set to the OURCE: * ... * ***** COCEM: CELIEF. ISON: FA. - 56 4. BA; OLD BILD SERMIT: IANTHAPE: English ANDMER 4 F 4 BIODIS MORYKIMET 2 4 FINALS . . Wari in Moore is hydrophilic successible, and regions in either Fig. of this frep should also be considered as potential . Therfere is to norm be specificity. Binding a tropposeint of . Type teint. ···interaction ··· sites tend to be modestly hydrathills, but als contain residues that could interact through the Lyar phoris effect. ACCESSION NUMBER: 1986:92387 BIOSIS DOCUMENT NUMBER: BA81:2803 ANALYSIS OF COMPUTER-GENERATED HYDROFATEY PROFILES FOR DITLE: HUMAN GLYCOFROTEIN AND LACTOGENIC HORMONES. KRYSTEK S R JR; REICHERT L E JR; ANDERSEN T T AUTHOR(S): DEP. BIOCHEMISTRY, ALBANY MED. COLLEGE, ALBANY, NEW YORK TORPORATE SOURCE: 12208. ENDOCRINOLOGY, (1985) 117 (5), 1117-1124. CODEN: ENDOAO. ISSN: 0013-7227. SOURCE: FILE SEGMENT: BA; OLU English LANGUAGE: -317(s)13L11 104 L7 S% L3 => d his FILE 'BIOSIS' ENTERED AT 17:21:56 ON 31 OCT 2000 3903 TWO HYBELD 1.3 7748 PROTEIN PROTEIN INTERACTION? 1.4 0 2 NEAF. 3 1129870 2 AND 3 687 L2 AND L3 L6 42849 MODULATOR OR EFFECTOR OR DISSASSOCIATOR L721 L6 AND L7 1.8 FILE 'BIGSIS' ENTERED AT 1":31:11 QU 31 ACT 2011 C LT(W) L3 : G 110 4 1. (5W) 1.5 1. 4 (7 8 1. or a few line as take ADDWER I OF 6 BIOSIS COTYRISHT 2000 BICCID Wentil Numlies an organ number reseptor that has been implicated in a river in-industible and appropriate that has been implicated in a river in-industible and propriate indication and indication and indication are indicated as property in the second of العد أرغ أرفة كرما الرفاء الراء والماد

Kang, Hy. - p.; fina, Mi-Ry und; hee, Sir-Ky p; Chin, Elf-Indi; Ci, Y m-Hee; Elm, Ne Sing; hee as Wi m ATTHE BOOK 11 Department of Microbiology, Institute for NERTHALE SIMECE: and Immunitedial Diseases, Yousei University College of Medicine, Secul, 120-75% South Korea Experimental No.1 Research, (May 1, 2010) Vol. 16, No. 11 1 114 15 pp. 545-554. 198M: (014-482) TEEN THE Article : An Walt: Fr. illish TERAKY DAN UWARE: Fr. illsn - A Rwin ibib dan HIP ANSWER 1 OF 6 BIOSIS COPYRIGHT 2000 BIOSIS Mir''' MOFI-B' is an orphan numbear receptor that has been implicated in ΛP activation-induced T-cell apoptosis. Retincids, potent immune ***modulators*** , were shown to inhibit the aptivation-induced appression of immature thymopytes and T-oqli hybriddmas. To illustrate the mechanism of the inhibition,. . . Nur'7 was significantly inhibited by cotransfection of RARalpha or RMRalpha. Nur" bound RARalpha or RMRalpha in both yeast and mammalian ***two*** - ***hybrid*** tests, suggesting that direct ***protein*** - ***protein*** ***interaction*** between these receptors may mediate the inhibition. Taken all together, we demonstrated that RA repressed Nur77 function through multiple mechanisms. . . ACCESSION NUMBER: 2100:242208 BIOSIS LOCUMENT NUMBER: PREV200030242203 Ratingia asid and its receptors repress the expression and transactivation functions of Nur77: A possible mechanism for the inhibition of apoptosis by retinoic acid. Kang, Hyo-Jin; Song, Mi-Ryoung; Lee, Soo-Kyung; Shin, AUTHOR(S):Eui-Chul; Choi, Youn-Hee; Kim, Se Jong; Lee, Jae Woon; Lee, Mi-Ock (1) (!) Department of Microbiology, Institute for Immunology CORPORATE SOURCE: and Immunological Diseases, Yonsei University College of Medicine, Seoul, 120-752 South Korea Experimental 2011 Research, May 1, 2000 Vol. 186, No. 3, COTECE: pp. 545-554. ISSN: 0014-4527. NOCUMENT TYPE: Article English LANGUAGE: SUMMARY LANGUAGE: English ANDMER . IF A PIODIC OFFEIGHT FOOT PIODIS

FOR DESCRIPTION OF THE FLAST OF MEN LAST OF SEPTEMBER OF THE PROPINCY OF THE PROPIN The control of the co rosepton embdimains are properly following and functional in the years. Basis Fur (FUF). . . . Supporting a define intil for heparin in 173F time firstion. Supporting a rat embryo CDMA library with bEGF in the yeast The second of th

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ar telin-protein intera PRESENTATION MERKS: : waa: ; = ; u; Remonstitution of fibroblast growth factor receptor · · · · · · · · · Enteractions in the yeast system. Al ni-Brinstein, Etnit; Sedim, Amirew; Yayon, Avmer (1 ATTHURST: A. Historias viii, come, search, and va, rayon, and to a long attent of Molecular Sell Bill gy, Weitmann Institute of Scheme, Behovot, "vi Israe.
Molecular Biotechnology, come, 1499° Voi. 11, No. 3, pp. THE HALL THE . # **** B. ** F : : STON: 1, ~3-(*** . LORDHALDT TYPE: Article : ANGWAGE: Edglish .TOMMARY LANGUAGE: English ANSWER - OF C FIOSIS CONVENENT 2001 BLOGIS . . unique binding partners and plays a distinct role in the cadherin-catenin complex. Using pl20 as bait, we conducted a yeast *****wo*** - ***hybrid*** screen and identified a novel transcription tartin which we named Kaisb. Kaisb's deduced amino acid sequence revealed an amine-terminal BTB/POZ ***protein*** - ***protein*** ***interaction*** | domain and three carboxy-terminal mino fingers of the C2H2 PNA-binding type. Kaiso thus belongs to a rapidly growing family of. . . It cadherin, or APC. like other POZ-MF proteins. Kalso localized to the nucleus and was associated with specific nuclear dots. Yeast ***two*** - ***hybrid*** interaction assays mapped the binding domains to Arm repeats 1 to $\ddot{7}$ of p120 and the carboxy-terminal 200 amino acids. . . heterodimerizes with PLZF. The involvement of FCZ-ZF proteins in development and cancer makes Kaiso an interesting candidate for a downstream ***effector*** of cadherin and/or p120 signaling. ACCESSION NUMBER: 1999:243790 BIOSIS PFEV139900248790 DOCUMENT NUMBER: The catenin P120ctn interacts with Kaiso, a novel BTB/POZ TITLE: domain zinc finger transcription factor. Daniel, Juliet M.; Reynolds, Albert B. (1) AUTHOR(S): (1) Department of Cell Biology, Vanderbilt University, 1161 21st Ave. South, Nashville, TN, 37232-2175 USA Molecular and Cellular Biology, (May, 1999) Vol. 19, No. 5, CORPORATE SOURCE: SOURCE: np. 3614-3623. issn: 0270-7306. Article POTUMENT TYPE: LANGUAGE: English SUMMARY LANGUAGE: English 110 ANSWER 4 OF 6 BIOSIS COPYRIGHT 2009 BIOSIS . . repears and an amino-terminal extension of 16 tandem leugine-rich repairs (1987). BE repeate form amphibatily fixtues structural units that realists output to bottom of the form of the control As a constant of the constant FULLER as bait identified a newel LER binding partner. The 1.15-Kilabase pair (kb) clone from the screen survived additional rounds of stringent inevera Pereni. Prindicka Pera i Pereni wase in merani make bikiyi in≔tomuk gase hipitati i s when Fir IFF. The translated corps to

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PRESIDENT TERMS NUMBER: the amount of this model of indicates : : : : : Jaitner, Birgit K.; Becker, Johns; Linnebann, In mas; ATTHER S Herrmann, Christian; Wittinahofer, Alfred; Elick, Christ gi To Fest Fach II us sa, 1-441.c Itermond Germany Journal of Biol gival Themistry, Nov. 21, 1980 Follows, No. 40, pp. John - From. Ison: 10-65-6 THE BATE OF THE i mara in hi Artinia. LAN CHARLE English - Extression librar? 521675 EXPRESSION 8185 EXPRESSIONS 526317 EMPRESSION (EXPRESSION OR EXERESSIONS) 35894 LIBRAR? 2253 EXPRESSION LIBRAR? 1.1.3 (EXPRESSION(W) LIBRAR?) - 1. armi 113 21 L2 AND L13 > d kwid tot 114 ANSWER 1 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS . . involves interactions between extracellular matrix proteins. To 23. identify proteins interacting with tuftelin, a potential nucleator of ename: crystallites, the yeast ***two*** - ***hybrid*** system was applied to a mouse tooth ***expression*** ***library*** and a tuftelin-interacting protein (TIP) was isolated for further characterization. Polyclonal antibodies were prepared against two recombinant variants of this. . 1.14 ANSWER 2 OF 21 BIDSIS COPYRIGHT 1990 BIOSIS . . specific association with other proteins. To discover proteins that AΒ. associate with hsp27, we made a differentiated rat Sertoli cell cDNA protein of 428 amino acids that we have named PASS1 (protein. . II ANSWER TO BIND OFFICE BUILD to hima or a somin sammar my sempombo nom i due o felfindati notatto dolo Librarano o elempotento e o elempariamento o celebrato no produce del materiale. . The many and denote the property of the prop Solitorsa och archypes ponter. The of MA was obtained to mean Solitors at that by the pompé intempressionité inflimentant py a fittwoite - tibybridite selection for a chas encoding calmodulin [CaM] = infina proteins. The predicte i protein is highly homologous to mammalian PETalpha, in What india after his tensency.

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yeas: ...w... - ...hybria... soreen: spreening methan Miscoliane us lescriptirs rainium-dependent omitular process; signaling pathway As N-terminal periods as a price to someon the human testis troughtest note to distrary to , we importing an angular echanical As New Fining, easy of a set pritoin Askiel, which consists it i, or and arris with an apparent molecular mass of. . . The ran-Western flotting and re-immunipresipitation assays demonstrate that the AR van interest directly with ARAICOTMF. Affinity gel pull-down and mammalian.w ... - ***hyprid*** assays further suggest androgen can enhance sluminicantly the interaction between AR and ARA166. Transient transferious assays deminstrated that ARAICS might. . . . og-immunitrecipitation: analytical method, presipitation techniques; reporter gene assay: genetic analysis, genetic method; transient transfection assay: Recombinant DNA Technology, genetic method; ***two*** - ***hybrid*** assay: genetic analysis, genetic method; S-protein affinity gel pull-down assay: activity assays, analytical method; Western blot: detection method, gene mapping, . . . ANSWER 6 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS Identification of a rice APETALA3 homologue by yeast ***two*** TI ***hybrid*** screening.

A JDNA clone OsMADS16 was isolated from the rice young inflorescence DDNA AB. ***hybrid*** screening method with OsMADS4 as bait. We have previously shown that the OsMADS4 gene is a member of the PI. . . expression patternsof the OsMADS16 and OsMADS4 genes are very similar to those of AF3 and PI, respectively. In the yeast ***two*** - ***hybrid*** system, OsMADS4 interacted only with OsMADS16 among several rice MADS genes investigated, suggesting that OsMAD\$4 and OsMAD\$16 function as a. Sequence Data

AFC:1766: DDMJ, EMBL, GenHank, amino acid sequence, nucleotide sequence

Methods & Equipment

two = ***hybrid*** screening: screening method

ANSWER 7 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
The yeast ***two*** - ***hybrid*** system has been used to identify A 13 mammalian clones that interact with policyirus 2A proteinase (2Apro). Eight glones which encode previously unidentified human proteins were Following American checker provides is undensitized named processing work species with the second section of the processing the second section in the second section of the second section in the second section is the second section of the second section of the second section is the second section of the sect

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····w··· - ···hykrid ...a nověl dene/protei system. lamily. Since 252-like protein . Hences are l prodicted to contain a coiled-coil domain, we used the yeast pull-a wh assays to investigate whether home- and in heteromeric nteractions (four tetween iffi-like proteins. Analyses of yeast. - like posstructe indicates on the Daj-like test of proteins interact in non-law one rate and a error of the contract of the letter that have an inequality askings the light their president coiled-roll demains. Similarly, entensive to the contract to the president subschings to a number president as produced interactors for both ADE, and ADE, and ADE, and ADE. Thus, In. -like proteins appear to exert and or . ARRWER 10 OF AL PIOSIS COPYRIGHT 2000 BLOSIS A 16-mar period library was screened using the yeas: ***two*** -*** typerid *** system to identity peptides which specifically interact with the human papillemavirus type 16 (HFV-16) E6 protein. Four different poptides were. . . an EL-LN-G motif. A fifth E6 binding poptide, derived from the putative tumour suppressor protein tuberin, was Identified during a ***two** - ***hybrid*** screen of a HeLa cDNA ***expression*** ***library*** . This people contained a Deletion metif. Henceldry to the peptides was found within the E6 binding proteins HoAP and Hé-Hi.. . . AMENER 11 OF .1 BIOSIS COPYRIGHT 2000 BIOSIS ****two*** - ***hybrid*** : So many interactions, (in) so little . . receptor-effector, as well as effector-effector, molecules of signal transduction pathways. Finally, assembly of transcriptional machinery involves protein interactions. The yeast ***two*** - ***hybrid*** method is a powerful technique for analyzing these protein-protein interactions. Since the publication of this technique in the late 1980s, the robust nature and far-reaching utility of yeast ***two*** -***hybrid*** systems for functional ***expression*** ***library*** cloning has led to the identification of many novel proteins in all areas of biological life science research. Additionally, ***two*** -***hybrid*** techniques provide a rapid and versatile system for the further characterization of discrete protein-protein interactions. Recent variations on the basic system have enabled application well beyond protein pairs, to investigate multi-protein complexes and protein-nucleatide interactions. Yeast - fittwofff - fitthybridfff motheds necessitate expression and subsequent interaction between a "protein of interest" functional pair within the yeast cell, uitimately driving reporter. . . gene expression and thus effectively linking protein-protein interaction(s) to a change in yeast cell phenotype. Functional protein-protein interactions using the ***two*** -***hybrid*** techniques have been demonstrated for all levels of Examinates nave peen demonstrated for all fevels of silling highly haven, until resently, extracellular protein-protein interest in more explicit from investigation with this terminate. Increasing the explicit from investigation with a trial extraction of the extr Methods & Equipment - ···expression··· - ···limrary··· cloning: bloning method; yeas: ***two*** = ***hybrid*** method: analytical method Miscollaneous Descriptors ention of mitting will added by light-respect interaction; protein-man destion interaction; protein-protein interaction; to be a considerable of the protein of the

. . that interest with the Artx. A proline-rish region of from a resembling an SHS-pinding distain was sed to screen an embryo olda. The expression of the e alpha-actinin. A yeast ***two*** - ***hybrid*** analysis showed a splinifier interaction between the prailine-righ region of SpCtm and a cutative SH: domain of the sea urchin. .. ANDWEB 14 08 31 BIOSIS NOPERIORI 331 BIOSIS
A trowgroup - troublisator system was used to someon years and human troppises form. The proteins that interact with mismatch repair proteins. FCNA was recovered from b. 'E illitaties and so wo in the Pase of. . . WARREN OF BI FIGSIS COPYRIGHT DOS BICKIS . . via the Hex and A-rax mutifs, we attempted to isolate prateins interacting with EBF-la 1% based on protein-protein interactions. A GLUA trempressioners tellibrary to trom wheat socilings was surgened with Sufficiently HPF-tacket, and a billetype protein, terme i HALF-1 (HBP-1-associated leucine-zipper factor-1), was isolated. GST-pulldown assay, yeast '**two*** - '**thybrid*** system and EMNA showed that FALF-1 and HBP1a(17 interact with each other through their leusine-migren regions. Dissection experiments showed that. . . 114 ANSWER 16 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS . . possibility that it has multiple roles in the viral life cycle. To A44 . obtain possible insights into these roles, the yeast ***two*** -***hybrid*** system was used to examine the interactions of the 52/55-kDa protein with viral and cellular factors. cDNA ***expression*** ***libraries*** from human 293 cells at both early and late stages of adenovirus type 5 infection were constructed and screened, with. . . . was shown to interact with a kacterial glutathione S-transferase-52/55-kDa fusion protein in vitre, further supporting the finding with the yeast - +**:wb+.. - ***nybrid*** system. Finally, coimmunoprecipitation studies confirmed that the 52/55-kDa protein and IVa2 polypeptide interact specifically during the course of adenovirus intection.. . . L14 ANSWER 17 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS A Hela SDNA ***expression*** ***library*** was screened for human AB polypeptides that interacted with the policyirus RNA-dependent RNA polymerase, 3D, using the ""two"" - ""hybrid"" system in the yeast Saccharomyces derevisiae. Sam63 (Src-associated in mitosis, 68 kDa) emerged as the human cDNA that, when fused. . . 1.14 ANSWER 18 OF 21 BIOSIS COPYRIGHT 10000 BIOSIS Miscellaneous Descriptors ENZYMES; GENE CLONING; HUMAN MYOTONIC DYSTROPHY; MEETING ABSTRACT; MEETING POSTER; MOUSE CARDIAC COMPLEMENTARY DNA *** EXPRESSION*** y, nina mamma. Pan aking usina si MA - titekpiniya utti - tita a satesitt in Jacobar Egyptic electricists.
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Forces white: this contains sensors for detection of analytes. *** District on the second of AMPARA - 15 - PICCIO COPPLIANT 100 FISSIO 119 AMSWER 7 OF 35 BLOSIS COPYRIGHT 2000 BLUSIS Ligand-dependent interactions of clastivators steroid receptor wactivator-1 and peroxiseme proliferator-activated receptor binding protein with nuclear hormone receptors can be imaged in live cells and are required for transtription. 519 ANSWER 8 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS Mitochondria-induced changes in intracellular pH regulate apoptosis. 1.19 ANSWER 9 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS A genetically encoded, fluorescent undicator for cyclic AMP in living L19 ANSWER 10 CF 35 BIOSIS COPYRIGHT MOOD BICSIS GFP-based optical recording from a C. elegans sensory neuron. L19 ANSWER 11 OF 35 FIGSIS COPYRIGHT MO00 BIGSIS Circular permutation and receptor insertion within green ***fluorescent ***prcteins*** 119 ANSWER 12 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS Assays for protein .inases using .**fluorescent*** ***protein*** substrates. 1.19 ANSWER 13 OF 38 BIDSIS COPMRIGHT 2000 BIDSIS Assays for protein kinases using fluorescent. T. I L19 ANSWER 14 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS New molecules to peak and poke at signal transduction. ΤΙ 119 ANSWER 15 OF 35 FIDSIS COPYRIGHT 2000 BIOSIS Dynamic redistribution of calmodulin in HeLa cells during cell division as revealed by a GFP-calmodulin fusion protein technique. CALL WER IN THE COLUMN TO EXPENSE OF New molecular semmers and oruginal perturbations to the that of the co-II. ANAWER I LE ELING TERRISIE - FEAR II. Maestrate standing two the territories in the electric territories of the ratio impains with samelessus. TIR ANDMER IN LE ME BILDIS CHETET MIT AND BILDIA NI Dynamic and grantifative Talk measurements usin Typamic and mantity ive Talk medicirements using imprived babelebus. 11 - Wilmer I - Le - El Dillo O Erriudio El Dillo El Dill

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- Green ***fluorescent*** ***proteins*** : Structures, photophysical ΤĪ mechanisms, and designed environmental sensitivities.
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- Structural basis for dual excitation and photoisomerization of the Aeguorea victoria green ***fluorescent*** ***protein*** .
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- Measurement and manipulation of cell signals with photons and designed ΤΙ molecules.
- 119 AMSWER 31 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
- Crystal structure of the Acquerea victoria green ***fluorescent*** ΤI ***protein*** .
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- Double labelling of subcellular structures with organelle-targeted GFF mutants in vivo.
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A" ****Tsien, Foto: Y. ... - MERRICHT I ENVIR Fig. respent Indicators in disding a pinding protein to lety, a deposi- $\mathbb{A}\mathbb{H}$ ***fluores.mnt *** ···fluoresaen···· protein molety has an analyte-binding region which binds an analyte and rauses the indicator to. . ITMajor Concepts Biochemistry and Molecular Biophysics; Methods and Techniques Chemicals & Biochemicals ***f!unfässent*** ***protein*** Methods & Equipment analyte detection: detection method; ***fluorescent*** ***protoin*** sensor: equipment ACCESSION NUMBER: 2000:283023 BIOSIS PREV200000288023 DOCUMENT NUMBER: ***Fluorescent*** ***protein*** sensors for TITLE: detection of analytes. ***Tsien, Roger Y. (1)*** ; Miyawaki, Atsushi ATTHUR SI: (1) San Diego, CA USA GORFGRATE SOURCE: ASSIGNEE: The Regents of the University of California PATENT INFORMATION: US 5998204 December 07, 1999 Official Gazette of the United States Patent and Trademark SOURCE: Office Patents, (Dec. 7, 1999) Vol. 1229, No. 1, pp. No pagination. e-file.. ISSN: 0098-1133. DOCUMENT TYPE: Fatent LANGUAGE: English >> file medline embase caplus File 'MEDLINE' FOURHED AT 17:47:18 ON 31 00T 7001 FILE THEFAMEL ENGREED AT 10:40:18 TO \$1 NOT jang di Kabupatèn Malabah B.W. Jawa di Bitu pelebah di FILE 'VELTO' BUTERED AT 11:4 :18 UP-1 UP-1 UP. OF INTEREST TO THE TERMON FOR THE CINCOLD THE ARESIDENT. CLEAR OR "HELE OVA STEPIN" FOR SETAINS. copyright of 200 americal chemical scolett add

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Answer it so tell MEDITUE Continue Continue the yeast of the order of the principal system and overlay assays we identified a putative ficinal of the first of the putation, which interacts with the GTE-bound forms to the and rack, but not with additionative home legies to shown proteins. The and rack, but not with additional including 4 leading original to show the indication of the first orser of an additional times of the putative of the forcest of the additional times this ment and displays a distinctive protein organization, thus.

ANSWER 162 OF 162 EMBASE COPYFIGHT 2000 ELSEVIER SCI. B.V.

AB ***Two*** ***hybrid*** species of hemoglobin M Iwate exist:
 .alpha.2(Mmet).beta.(met).beta.(deoxy) and .alpha.2(Mmet).beta.2(deoxy).

These species differ in their ligand and ***effector*** binding properties. The .alpha.2(Mmet).keta.(met).beta.(deoxy) hybric is sharatterined by a Pohr effect, while the Hill boofficient is n=1.00. The energy of. . .

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122 ANSWER 1 OF 162 CAPLUS COPYRIGHT 2000 ACS

The invention concerns a method for yeast screening of protein-kinase AB modulators specific for higher eukaryetic cells, including human cells, characterized in that it consists of: (a) expressing the substrate(s) of said protein-kinases and the interacting partner(s) specific for said protein-kinase substrate(s) in a double-hybrid system in Sacrharonyces cerevisiae in a selective fulture medium in the presence of potential inhibiting agents of phosphorylation-dependent interactions of said substrate(s) with their specific partners; (b) screening in said double-hybrid system for said protein-kinase inhibitors; and (c) detg. the specificity of the inhibitors obtained in step (b) by reaction with an antibody specific for the phosphorylated form of the substrates. Thus, the method was demonstrated using the interaction of I.kappa.B.alpha. (tused to the Gal4 transactivation domain) with human .beta.TrCF (fused to the LexA CNA-binding domain). An antibody specific for phosphorylated I.karpa.B.alpha. indicated that I.karpa.P.alpha. was phosphorylated in Dischargeyees forevisiae, even though yeast gentains no protein kinase The equation of the Committee of the Com

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The invention provides a method for someoning new bic-active mols. for the ability to affect the interactions of proteins or other mols., whereby the interactions of said proteins/mols. are detected in vivo or in vitro. The method of the invention begins with the construction of DNA libraries which represent the collective genomes of naturally occurring microorganisms archived in cloning vectors that can be propagated in suitable prokaryotic hosts. Such microorganisms are preferably extremophiles, such as hyperthermophiles, ***psychrophiles*** psychrotrophs, halophiles, and acidophiles. The method further involves contacting a bio-active compd. isolated from said library with a test protein linked to a DNA binding moiety or a second test protein linked to a transcriptional activation moiety and detg. the ability of said compd. to regulate the interaction of the first protein with the second, wherein said regulation enhances or inhibits the expression of a detectable protein. The invention offers the ability to screen for many types of bio-active compds., particularly those which are enhancers and inhibitors of protein-protein or other interactions, such as those between transpription factors and their activators or receptors and their cognate targets. In one embodiment, the methods are directed toward the discovery of possible antibiotics, anti-virals, anti-tumor agents, and regulatory proteins.

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Random sequencing of cDNA and ***genomic** ***libraries*** has been used to study the genome of the hyperthermophile Thermotoga maritima. To date, 175 unique clones have been analyzed. . . 18 trpG and 14 trpD genes from other organisms suggest that the Thermotoga trp genes resemble corresponding genes from other ***thermophiles*** more closely than expectable.

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AB . . . hypridized with LNA fragments from four symmobacterial species. The genes moding for subunits I and II were cloned from the ***genomic*** ***library*** of the thermophilic dyanobacterium S. vulcanus, and the nucleotide sequence of the subunit II gene was detd. The deduced protein. . . subunit IIs. The S. vulcanus subunit II does not contain the hytoshrome a molety that is present in bacilli and ***thermophiles*** .

1.31 ANSWER 9 OF 10 BIOSIS COPYRIGHT 2000 BIOSIS

Studies of the hyperthermorphile Thermotoga maritima by random sequencing of cDNA and ***genomic*** ***libraries*** : Identification and sequencing of the trpEG (D) operon.

AB Random sequencing of cDNA and ***genomic*** ***libraries*** has been used to study the genome of the hyperthermophile Thermotoga maritima. To date, 175 unique clones have been analyzed. . . 18 trpG and 14 trpD genes from other organisms suggest that the Thermotoga rp genes resembled corresponding genes from other ***thermophiles*** more closely than expected.

131 ANSWER 10 OF 10 PIOSIS COPYRIGHT 2000 BIOSIS

AB. . . with DNA fragments from four dyanobacterial species. We have closed the genes coding for subunits I and II from the "**genomic***

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lagy institute, University TREBATE CITE T: 19931 Journal of Molecular Biology, (THE TER issn: 3122-2446 inden: omléák 1 4 11 1 RY: United Kingdom Journal; Artible 334 Mibrobio : TIME TIES: Microbiology Clinical Fiochemistry HILL SEGMENT: 029 TANAMATA Enulish COMMANY LANGUAGE: English Rand m sequenting of CMMA and """proceed """ ***librari@s*** has iven uses to study the senome of the hypertherm phile libermothing maritims. To date, I is unique clones have been analyzed by comparing short sequence tags with known grateins in the HIR and backard detabases. We find that a significant proportion of sequences can be may heard previously identified proteins from non-Thermotoga sources. A high match rate was obtained from an eligo dT'-primed oENA library, where ene-third by all unique sequences analyzed (21/60) shared high amine acid sequence similarity with proteins in the PIR and GenBank databases. Also, approximately one-third of the unique sequences from a second cDNA library (28/89), constructed with random oligo primers, could be matched to sequences in FIR and GenBank. Identification of genes from the oligo,dT)-primed cDNA library indicates that some Thermotoga mRNAs are polyadenylated. Genes have also been identified from a 1 to 2 kb genomic DNA library. Here, (3/21) of genomic sequences analyzed could be matched to proteins in PIR and GenBank. One of the genomic clones had high sequence similarity to the tryptophan synthesis gene anthranilate synthase component I (trpE). Using this sequence tag, the Thermotoga trp operon was isolated and sequenced. The Thermotoga maritima trp operon is arranged with trpE forming an overlapping transcript with a second protein consisting of a fusion of anthranilate synthase component II (trpG) and anthranilate phosphoribosyltransferase (trpD). With regard to the fusion, the operon organization is similar to Escherichia coli and Salmonella typhimurium, but lacks the classic attenuation system of enteric bacteria. Amino abid sequence comparisons with 19 trpE, 18 trpG and 14 trpD genes from other organisms suggest that the Thermotoga trp genes resemble corresponding genes from other ***thermophiles*** more closely than expected. 131 ANSWER 2 OF 10 EMBASE COFYRIGHT 2000 ELSEVIER SCI. B.V.

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characteristics of the deduced protein sequence for subunit

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OFME, 11846 Mor 210 185 Tel. 1868: 125-1115. ATTH #: Notherlands 179. 177.1991 Journal; Artiole; (NOTEMAL ARTICLE) LANGUAGE: English Priority Journals FILE SEGMENT: THEE SOURCE: GENBANK-185038 HITRY MONTH: 199703 A hyperthermophile NC12 was newly isolated from Noboribetsu hot spring. To characterine this organism, a gene coding for 168 rRNA was cloned and sequenced. The 16S rRNA sequence from MC12 shows the highest similarity with those from Pyrodictium occultum and Desulfurococcus mobilis among the sequences in the database, inducating that NCIA belongs to a cluster of extreme ***thermophiles*** (Crenarchaecta) in the archaeal domain. However, since the highest identity score was only 91.2%, it is suggested that NC1, may oppositute a new gents 131 ANSWER 4 OF 19 MEDLINE ACCESSION NUMBER: MEDLINE 93294870 DOCUMENT NUMBER: 93294870 TITLE: Studies of the hyperthermophile Thermotoga maritima by random sequencing of cDNA and ***genomic*** ***libraries*** . Identification and sequencing of the troEG (D) operon. Kim C W; Markiewicz F; Lee J J; Schierle C F; Miller J H AUTHOR: Department of Microbiology and Molecular Genetics CORPORATE SOURCE: University of California, Los Angeles 90024... JOURNAL OF MOLECULAR BIOLOGY, (1993 Jun 23) 231 (4) 960-81. SOURCE: Journal code: J6V. ISSN: 3022-2336. ENGLAND: United Kingdom FUB . COUNTRY: Journal; Article; (JOURNAL ARTICLE) LANGUAGE: English FILE SEGMENT: Cander Journals; Friority Journals GENBANK-A30904; GENBANK-J01511; GENBANK-M33814; OTHER SOURCE: GENBANK-M36636; GENBANK-M55911; GENBANK-M65060; GENRANK-M93788; GENBANK-S66091; GENBANK-M04960; GENBANK-X17149; GENBANK-X57853; PTR-A22626; PIR-A35116; PTR-A35250; FIR-A35989; PTR-P2498; PTR-B32640; PTR-C351 LIB-ESSION, DIE-ZHOOMS, DIE-TWOONS, DIE-SONSTON, DIE-SONS Baran sepending i SWA and it the bold in o trouil adio. tro cas ion isomit study the sense of the hypertherm pile likers to be satisfied. It sate, it is made to be not seen analysed at organic state of at we set to take with known proteins in the Hib and Achbank is anases. We find that a simificant proportion of sequences can be matched to providually

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31 ANSWER 5 OF 10 MEDLINE

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Department of Applied Chemistry, Fagulty of Colenne and MORECHATE SOURCE:

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Blue-green algae (cyanobacteria) contain both primitive photosynthetic and respiratory systems in their membranes. The controversial genes coding for an alpha alpha 3-type cytochrome oxidase in cyanobacteria were examined. The DNA probe coding for the most conserved part of subunit I hybridized with DNA fragments from four cyanobacterial species. We have blened the genes coding for subunits I and II from the ***genomic***

library of the thermophilic cyanobacterium Synechococcus vulcanus and determined the nucleotide sequence of the subunit II gene. The deduced protein sequence (327 amino acid residues) indicates that there are two hydrophobic segments near the N-terminus and a hydrophilic intermembrane demain containing ligands for CuA (the ESR-active Copper) similar to other subunit IIs. The S. vulcanus subunit II does not contain the cytochrome c moiety that is present in bacilli and ***thermophiles***

131 AMSWER 6 OF 10 CAPLUS COEYRIGHT 2002 ACS 1998:547256 CAPLES ACCESSION NUMBER:

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Screening of a fosmid library of marine environmental narymi : PNA tramments revosis four closes related to

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Kim, Choll Man; Markiewicz, Peter; Iee, Jean J.; Schierle, Clark F.; Miller, Jeffrey H. Mil. Piel. Inst., Univ. Calli Inia, Los Andeles, JA, 1. Mel. Piel. 1983, vol 4., 860-61 COPEN: UMOBAK; ISSN: 1-02-1886 THE BAIR ONE TE

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peen used to study the genome of the hypertherms; hile Thermotoga maritima. To date, I'm unique michos have been analyzed by comparing short sequence tags with shown proteins in the FIR and GenBank databases. The authors find that a significant proportion of sequences can be matched to previously identified proteins from non-Thermotoga sources. A high match rate was obtained from an eligo(dT)-primed cDNA library, where one-third of all unique sequences analyzed (21/65) shared high amino acid sequence similarity with proteins in the FIR and GenBank databases. Also, approx. one-third of the unique sequences from a second cDNA library (28/89), constructed with random cligo primers, could be matched to sequences in FIR and GenBank. Identification of genes from the oligo(dT)-frimed dDNA library indicates that some Thermotopa mRNAs are polyadenylated. Genes Late also keen identified from a 2 to 2 kb german DNA library. Here, (3/21) of genemic sequences analyzed could be matched to proteins in PIR and GenBank. One of the genomic clones had high sequence similarity to the tryptophan synthesis gene anthranilate synthase component I (trpE). Using this sequence tag, the Thermotoga trp operon was isolated and sequenced. The Thermotoga maritima trp operon is arranged with trpE forming an overlapping transcript with a second protein consisting of a fusion of anthranilate synthase component II (trpG) and anthranilate phosphoribosyltransferase (trpD). With regard to the fusion, the operor organization is similar to Escherichia coli and Salmonella typhimurium, but lacks the classic attenuation system of enteric bacteria. Amino acid sequence comparisons with 19 trpE, 18 trpG and 14 trpD genes from other organisms suggest that the Thermotoga trp genes resemble corresponding genes from other ***thermophiles*** more closely than expected.

131 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2000 ACS

1993:2868 CAPLUS ACCESSION NUMBER:

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The dynochrome doxidase genes in blue-green algae and

characteristics of the deduced protein sequence for subunit II of the thermophilic cyanopacterium

Synechococcus vulcanus

Tano, Hiroyufi; Ishimuka, Miric; Sone, Mobuhito ATTHUR (* : Fig. Sci. Fna., Thu Chiv., Tokyo, 112, Japan F. Men. Hi phyo. For ... I or m. I dell, Japan F. Men. Hi phyo. For ... I or m. I dell, Islaid, Islaid. THE BATE ATER:

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erin. An - 1 ; Markiewich, Peter; Jees, AUTHOR, J.: Mol. Biol. Inst., Dep Microbiol., Univ. California, GREERATE ESTROE: Angles, CA 90024 USA Journal of Molecular Biolegy, [1-93] Vol. 131, No. 4, FF. 960-981. 120-2638. Iden: f CATTMENT THE Article En filet AND A HELD been used to study the genome of the hypertherm pulle Thermotora maritima. To date, I'm unique clones have been analyzed by comparing short sequence twis with known proteins in the FIE and DenHank databases. We find that a significant proportion of sequences can be matched to previously identified proteins from non-Thermotoga sources. A high match rate was orkaines irim an chigo all eprimed pRNA library, where che-third of all unlique segmentes analyzed (21/6) shared high amine adid sequence similarity with proteins in the FIR and Genhank databases. Also, approximately one-third of the unique sequences from a second cDNA library (28/83), constructed with random oligo primers, sould be matched to sequences in PIR and GenBank. Identification of genes from the c.lg:[il]-primed :DNA library indicates that some Thermotoga mFNAs are polyadenylated. Genes have also been identified from a 1 to 2 kb genomic DNA library. Here, (3/21) of genomic sequences analyzed could be matched to proteins in PIR and GenBank. One of the genomic clones had high sequence similarity to the tryptophan synthesis gene anthranilate synthase component I (trpE). Using this sequence tag, the Thermotoga trp operon was isolated and sequenced. The Thermotoga maritima trp operon is arranged with trpE forming an overlapping transcript with a second protein consisting of a fusion of anthranilate synthase component II (trpG) and anthranilate phosphoribosyltransferase (trpD). With regard to the fusion, the operon organization is similar to Escherichia coli and Salmonella typhimurium, but lacks the classic attenuation system of enteric bacteria. Amino acid sequence comparisons with 19 trpE, 18 trpG and 14 trpD genes from other organisms suggest that the Thermotogu rp genes resembled corresponding genes from other ***thermophiles*** more closely than expected. L31 ANSWER 10 OF 10 BIDSIS COPYRIGHT 2000 BIOSIS ACCESSION NUMBER: 1991:76632 BIOSIS DOCUMENT NUMBER: BA91:45087 THE CYTOCHROME COMIDASE GENES IN BLUE-GREEN ALGAE AMD TITIE: CHARACTERISTICS OF THE DEDUCED EFOTEIN SEQUENCE FOR SURFAILT II OF THE THERMOPHILIC CYANOBACTERIUM SYNECHOCOCCUS-VULCANUS. TANO H; ISHIZUKA M; SONE N AUTHOR(S): THE APPLIED CHEMISTRY, FACULTY SCIENCE ENGINEERING, CHUC THILDEBUILTY, HALLY WAS BUILDED -FOUNDER THE TELL OF THE PROCHEM PROPERTS RES COMMUNICATION TO THE TELL ASSESSED. OH TANK I OF THE TOPES BER WELL LAND: · 1/2 Fig. 1/2 Fig. 1 PA; A. 4. . AB - Blue-green as pag coyanobacteria contain between milities plus esymmetic and respiratory systems in their membranes. The controversial memory builts for an aas-type cytochrome exidase in cyanchasteria were examined. The LWA print the most conserved part of schools I hybridized with DNA transport troops to you have the present and the property of th in the contract of the second second

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. . . positive selection for mutants of the human historic hairpin-binding protein (HHF) papable ': interacting with non-panchis. hairping and in a ''thegative'' '*'selection''' for loss-of-binding mutants. Interestingly, all mutations from the positive solection are iscated in the N- and C-terminal regions flanking a. . .

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ANSWER 2 OF 4 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V. DUPLICATE 1 New tools for protein linkage mapping and general ***two***

hybrid screening.

The ***two*** - ***hybrid*** system has proved to be a facile method AΒ for detecting and analyzing protein-protein interactions. An expanded application of this system,. . . new strains and vectors that will allow for more efficient screening. The strains contain a GAL1-URA3 reporter for positive and ***negative*** ***selection*** , as well as a UAS(G)-lacZ reporter. The strains are of opposite mating types, permitting libraries present in one strain to. . . plasmids, despite significantly lower protein levels. In addition to protein linkage mapping, these reagents should be generally useful in standard ***two*** - ***hybrid*** applications.

AMSWER 3 OF 4 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.DUPLICATE 2 Genetic characterization of a mammalian protein-protein interaction domain ry using a yeast reverse '**'two*** - **'hybrid*** system. . . . protein-protein interactions to be selected from large libraries of randomly generated mutant alleles. The strategy, based on a yeast reverse ***two*** - ***hyprid*** system, involves a first-step ***negative*** ***selection*** for mutations that affect unterson in, i ii wa ky a zero mezie przezione zale mi in fara zakiet treze mirat, no that maintain expressi n. . . . i faltetati d. line two-group zele mi fagit terme can be un i to distributed any interacti n a mun tent can be to tea le the continue of the continue any interacti n

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Vidua M.; Brown F.; Chen E.; Broke J.I.; Harlaw E. AUTHOR:

Building 149, Massachusetts Gen. Hosp. Cancer Ctr., lath CORPORATE SOURCE:

Street, Charlestown, MA 02129, United States

Proceedings of the National Academy of Sciences of the SOURCE:

United States of America, [1996] 93/19 (10321-10326).

ISSN: 0027-8424 CODEN: FNASA6

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133 ***Short, Jay M.***

. . . single-chain antibodies. Shuffling can also be used to recombinatorially diversify a pool of selected library members obtained by screening a ***two*** - ***hybrid*** screening system to identity library members which bind a predetd. polypeptide sequence.

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L43 ANSWER 1 OF 2 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V. The interaction of apocalmodulin (apoCaM) with a peptide (Neuro(p)) based AB on the primary sequence of the calmodulin-binding domain of neuromodulin has been studied by nuclear magnetic resonance (NMR) methods. The NMR spectra of both apocalmodulin and its 1:1 complex with the Neuro(p) peptide have been assigned by triple resonance and nuclear Overhauser effect- MOE- hased strategies. ApoCaM displays many of the same basic structural features as calcium-saturated calmodulin. Analysis of observed chemical shifts and patterns of MOEs on the main chain indicates extensive and regular secondary structure throughout the N-terminal domain. In contrast, the helices of the C-terminal domain are somewhat irregular and are dynamically averaged. The EF-hands are intact in the N-terminal domain with the loops forming a short antiparallel .beta. sheet. Under low-salt A first has, by the limest opened in PFE hand notified are present in the terminal armain of approximation of the permit of t posed in at 1 mg of a postablog in a my loward in with the Neuron pospetise are as a carbon by small with the carbon memoral unity part areas in a padratic of the tereminal dimain. The meneral secondary structure and testilary organization appears to remain roomly the James as in the application Statistic metric tirration of the appCaM. This Libeuro 'p' complex with paloium indicates that the C-terminal domain FF-hands have a higher affinity for calcium than N-terminal domain EF-hands. Thus, this complex offers a unique appointmitty to examine the attractural and energetic throughout to calling diponent and cart what problems in indicated rent place to the more about.

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           Journal of Neuroscience Research, (1997) 48/5 (407-424).
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            Refs: 37
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            . . . is involved in the CNS, we screened molocules that directly
           associate with Fyn in neonatal mouse brain by using a ***two*** -
              ***hybrid*** yeast system. We isolated five cDNA clones with strong and
            reproducible Fyn-binding activity. Sequence analyses revealed that three
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           Medical Descriptors:
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146 AMSWER 1 OF 681 CAPLUS COPYRIGHT 2000 ACS ACCESSION NUMBER: 2000:283960 CAPLUS DOCUMENT NUMBER: 132:315571 Identification and comparison of ***protein*** - ***protein*** and TITLE: identification of inhibitors Nandabalan, Krishnan; Rothberg, Johathan Mars; Yang, INVENTOR(S): Meijia; Knight, James Robert; Kalbfleisch, Theodore Samuel Curagen Corporation, USA FATENT ASSIGNEE(S): U.S., 161 pp., Cont.-in-part of U.S. Ser. No. 663,824. SOURCE: CODEN: USHXAM FOCUMENT TYPE: Patent .ANGTABE: Enallsh FAMILY ACT. NUM. OF MIT: FATENT INFORMATION: rangers and grain name APPLICATION NO. LAWF

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a diverser of the transmembrane receptor Til., I real also diated in miltory plasming trainmikity: the Danus and embryo the nucleus. Ture and Pelle are required to relay the signal from Toll to the Dersal-Captus complex. In a yeast - firthworth - firthybridity - assay, we found that both Tube and Pelle interact with Porsal. We confirmed these interactions in an in vitro binding. . . Medical Descriptors: *embryo development signal transdubtion protein targeting cell rucleus - * * * rrotein protein interact.on * * * drosophila nenhurar. embry: articlo priority fournal *protein *polymer membrane receptor ANSWER 2 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V. A yeast genetic system for selecting small molecule - ***inhibitors*** of ***protein*** - ***protein*** ***interactions*** in nanodroplets. Proceedings of the National Academy of Sciences of the United States of America, (1997) 94/25 (13396-13401). Refs: 49 ISSN: 0027-8424 CODEN: PNASA6 . . networks of molecular interactions. Dissection of their role most AB commonly is achieved by using genetic mutations that alter, for example, ***protein*** - ***protein*** ***interactions*** . Small molecules that accomplish the same result would provide a powerful complement to the generic approach, but it generally is. . . polymer beads. Here, we describe a genetic system compatible with split-peal synthesis that allows the describe to reli-perceable, enable relevants with interest to the compatible with split-peal synthesis that allows the describe to reli-perceable, enable relevants with the constraints of the compatible with split-peak synthesis that allows the describe the compatible with split-peak synthesis. self biltuin ing lets, karpanea ky a ne entry are marea termilape inat arrago caracidezdo en el vilhon poeto interactina perteino atter unaimum ministratam se whise interaction is runt. In vill state in the present of the control of the analysis are the control of the orthybridees assay . Disruption of the interaction by a small more will all was growth, and the small molecule can be into dured into the. . . This system should provide a mondral mothod for releasing coll-permeable Clianus that can be used to strong the relevance of ottp: teintto — Ottp: point; Modification of the second

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ANYWER II OF SHEEMBASE PERIORS . TO FINENIER SOLE B.V. . . twin that interacts with the multifunctional Murlein Arias Research, (1997 1994 1946-1949). Best 8: 44 m: Us Tel 4e Alfri MARHAI . . . might mediate the function/stability of YYI in muscle wells, we spreened an adult numan muscle DDNA library using the yeast ···hybrid··· blening system. We report the isglation and sharasterization of a novel protein termed YAFZ (YY1- associated factor 2 - Heavang of YYI by the calcium-abtivated protease inat interacts. . . m-valpain. The isolation of YAF, may help in understanding the mechanisms through which thinking terms to a my senior transcription may be astaminised in eliminated by prite lysis during mastle perelopment. Medital Descriptions: tagto istlāti ir *muscle development *transpription regulation amine acid sequence amiro terminal sequence animal tissus article coll differentiation win'railed study una library dna transfection molecular cloning muscle cell myoblast newborn nonhuman nucleotide sequence priority journal promoter region protein degradation ***protein protein interaction*** rat yeast *transcription factor *zino finder protein basic protein calpain lysine messender rha: EC, endogenous compound AMOWER 12 OF 33 EMBASE COPYRIGHT 2000 ELSEWIFR SCI. B.V. 11.1. Wille, 1.4.1. 14.1. 1.1. 1.1.1. 1.1.1. F-18: 31 1.10%: ----THE COURT Appage - time tit = tithpe, Att - chemical lentitle filletta a b readstription factor repails of interacting with the posset protein tamily. We show that Heffi . . . An artivation domain. CAI4-funion experiments indicate that HEFF contains a masked activation domain. Deletion of two independent N- and C-terminal - ***inhibitor*** - domains unmases an artivation demain which is lighted more active than the full remark project. The released activation organity is. . . White the string of the section

protesta demain protein randly structure antivity relation. thian mobility arous protein tretin plast ma protein thansmighten factor *virus gritoin protein ANYWER IS FOR SELECTION OF THE OUT OF SELECTIONS OF THE PARTY. sm pagene, (1997) 14-14 (144-41) 4). Refs: 23 ... 1780: 181-9.31 OCCEN: ONCHES 1771: principals - Tritagetti - Tritagerlatit - System we have laborible a novel retential Cdk4 interacting proteins. Here we described the irteraction Tak4 with a human homologue of . . . Tik6, but not with Codz, Tuk2, Tak3, Cok5 and any of a number of syclins tested. Cic5 is not an ***inhibitor*** nor an activator of the Cdk4/cyclin D1 kinase, while it appears to facilitate complex assembly between Cdk4 and cy lin 01. . . Mcdical Descriptors: artiale romplex formation dresophila humar. human cell priority journal protein assembly ***protein protein interaction*** sequence homology reall cycle protein: EC, endogenous compound *cyclin dependent kinase: EC, endogenous compound avaline: EC, endogenous compound ANSWER 14 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V. 1.47 EMBO Jaurnal, (1993) 16/6 (1413-1426). R∈fs: 63 ISSN: 0261-4139 CODEN: EMJODG We have isolated a human cDNA which encodes a novel I.kappa.B family AΒ member using a yeast ***two*** - ***hybrid*** screen for proteins able to interact with the p52 subunit of the transcription factor NF-.kappa.F. The protein is found in. . . give rise to a protein of $45\,$ kPa, which exists as multiple phosphorylated isoforms in resting cells. Unlike the other $\raisetation***$, it is found almost exclusively in complexes obstaining RelA and/or cRel. Upon activation, 1.kappa.B-.epsilon. protein is degraded with slow kinetics. . . Media d Desertrers: tratte in the interest aantelootani y Siiniga jiesso pasielootea ah osotti ardin territorio de pessoa against be grants attack to a lumār. kinetias nydl y iesia

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the yeast offitwatto - fitthyrriditt system was used to is late
      S.pombe oDNA slones enguing proteins that interact with Niml. Sixteen %:
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      tantimitotic agent: EG, endogenous compound
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     ANSWER 16 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
     Inactivation of the cdk \star\star\starinhibitor\star\star\star p27(KIP1) by the human
     papillomavirus type 16 E7 oncoprotein.
      Oncogene, (1996) 13/11 (2323-2330).
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      Refs: 41
      ISSN: 0950-9232 CODEN: ONCNES
      . . . loss of cell adhesion, two experimental conditions in which cell
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        ple progression is accompanied by elevated levels of the odk
      ***inhibitor*** p27(KiPl). We show here that E7 can antagonize the ability of p27(KiFl) to block cyclin E-associated kinase in vitro and.
      . association requires the C-terminal part of ET. The interaction between
      p27(KIP1) and E7 can also be demonstrated in a yeast ***two*** ***hybrid*** system. The data suggest that the ability of E7 to override
      certain forms of G)/G1 arrest is mediated in part by binding to and
      subsequent inactivation of the adk ...inhibitor. p27(KIF1).
     Medical Descriptors:
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conserved region or p21 _{\odot} inc acids 46-740, which is homosimilar regions in the resided Cdk _{\odot} ***inhibitors*** p2
     However, the site's on. . . molecules with various N-terminal and
     P-terminal selections and tested each for their addity of kins of $10 49 the yeast of the edgains assays.
     None or the deletion mutants tested found to p. 1 by Wither assay. We new tested whether p21 could kind to lak , a component if the
      yolin-activating kinase complex. By both the double-tagging and years
       ********* - ***hybrid*** &seays, p. 1 fallog to kind to this protein,

    nelstent with previous reports. However, hybrid molecules consisting of

     the amin -terminal half. . . Furthermore, the yeast CdvNA protein, which is similarityal with Ydk2, railed to bind to pilky both the yeast
       but not Jdn.+00iki hýbřids s pid niná té pil. These results su mest that
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     ANSWER 18 OF 33 EMBASE COFYRIGHT 2000 ELSEVIER SCI. B.V.
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     RhoGDI-3 is a new GDP dissociation ***inhibitor*** (GDI):
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     Identification of a non-cytosolic GDI protein interacting with the small
     GTP-binding proteins RhoB and RhoG.
      ournal of Biological Chemistry, (1996) 271/48 (30366-30374).
     ISSN: 0021-9258 CODEN: JBCHA3
     . . . endogenous RhoB protein is regulated during the cell cycle,
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     contrasting with the permanent RhoA protein expression (1). Using the
     interacting with RhoB, we identified a new mouse Rho GDP dissociation
       ***inhibitor*** , referenced as RhoGDI-3. The NH2-terminal a helix of
     RhoGDI-3 is strongly amphipatic and differs thus from that found in
     previously. . . acting on Rab or Rho, RhoGDI-3 is associated to a Triton X-113- insoluble membranous or cytoskeletal subcellular fraction.
      In the " **** wo*** - "**hybrid*** system, RhoGD1-3 interacts
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Researchy, the critical in system has been extended to it denome-wide marring of the critical interpolation. . io : ::gen me-wide mapping of f protein interactions. In addition, immunophilins and their chem lidans are provising useful reagents for penerating a naitional attended to the state of the sta dissent intracellular signaling pathways. Medical Descript rs: · · · · protein protein interaction · · · picalemistry dimerication. dene mapping monet Readpender aten. * 178 ni, nii lan ân primity bornal protein acmain smirt survey signal transduction dna binding protein immunophilin peptide ANSWER 20 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V. 1.4° Molecular and Cellular Pinlogy, (1996) 16/11 (555)-5864). ISSN: 0200-0308 CODEN: MCEBD4 AΒ The E1B 19-kilodalton protein (19K protein) is a potent apoptosis ***inhibitor*** and the adenovirus homolog of Bcl-2 (E. White, Genes Dev. 18:1-15, 1996). To obtain a better understanding of the biochemical. . . which interact with E1B 19K and Bcl-2 and promote apoptosis. Like Bax and Bak, Nbk was cloned from a yeast ***two*** - ***hybrid*** screen for proteins that interact with E1B 19K. Nbk contained BH3 but not BH1 or BH2. It also interacted with. . . apoptosis. Nbk may therefore represent a novel death regulator which contains only a BH3 that interacts with and antagenizes apoptesis ***inhibitors*** such as the E1B 19K protein. Medical Descriptors: *apoptosis ****protein protein interaction*** animal cell article molecular cloning nonhumán. priority (durna) protein family protein industion protein legalization 11:1 then profit tra talin i di protein ram 11 10 1 . 1 ANSWER 21 OF 33 EMBASE COPYRIGHT LONG RUSEVIEW SOL. F.V. Vectors for a 'double-targing' assay for of the CIFC-tinding domain of homes. 4 de , 1 de 1 de 1 de 14 de 14 de 15 d Transfer de 15 de 15

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     Inveragion between Fish and - *** inhibit prs*** - In will division.
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     The interaction between "trinhibitors:" at well division and Fish were assessed by using the yeast "triumptor" - "trinhibitors. An
     interaction was observed between FisZ and SulA, a component of the Suc
     response, and the interacting regions were. . .
     Medical Descriptors:
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     ANSWER 23 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
     Science, (1996) 272/5265 (1179-1192).
ISSN: 0036-8075 CODEN: SCIEAS
     . . . kinase (MAPKKK) family, TAK1, was previously identified as a
AB
     mediator in the signaling pathway of IGF-.beta. superfamily members. The yeast ***two*** - ***hybrid*** system has now revealed two human
     proteins, termed TAB1 and TAB2 (for TAK1 binding protein), that interact
     with TAK1. TAB1 and TAK1 were co-immunoprecipilated from mammalian cells.
     Overproduction of TAB1 enhanced activity of the plasminogen activator
       ***inhibitor*** 1 gene promoter, which is regulated by, TGF-.beta., and
     increased the kinase activity of TAKI. TABI may function as an.
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            interactions in vivi. We find that distinct a mains in rebel and vebel are
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TI A23, an "Tinhibitor" of dell beath, self-associates
                                                                             of cell death, self-associates by its wind
           finger domain.
            FEBS Lettors, (1996) 384/1 (67-64).
            ISSN: 0014-5793 CODEN: FEBLAL
            . . . rells. The A20 protein belongs to a novel class of Cys2/Cys2 zinc
           finger proteins, and has been characterized as an ***inhibitor*** of
           both aportotic and necrotic cell death. In order to clarify its molecular
           mechanism of action, we used the yeast-based ***two*** - ***hybrid*** system to screen for A20-associated proteins. Here we report that A20 is
           able to self-associate, and demonstrate that the latter.
           Medical Descriptors:
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luentification of a nuclear-specific cyclophicin which interacts with the
proteinase ***inhibitor*** eqlin c.
Biochemical Journal, (1996) 314/1 (313-319).
ISSN: 0264-6021 CODEN: BIJOAK
We have identified a novel human cyclophilin (hCyP-60) which interacts
with the proteinase ***inhibitor*** eglin c using the yeast
    ****two*** - ***hybrid*** system. A cDNA isolated from a Raji B
 lymphocyte library reveals a domain showing sequence similarity to known
dydlophilins flanked. .
Medical Descriptors:
    *** protein protein interaction ***
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94... INCHES se.. population dria damade dna replication endine linked impuntsorbent assay hunar human tissue immunoprecipitation mammal dell mouse nonhuman priority. . . ANSWER 19 OF 35 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V. Interactions among members of the Bol-2 protein family analyzed with a yeast *** - ***hybrid*** system. Proceedings of the National Academy of Sciences of the United States of America, (1994) 91/20 (9238-9242). ISSN: 0027-8424 CODEN: PNASA6 . . . with itself and other members of the Bol-2 family, including Bcl-X-L, Bcl-X-S, Mcl-1, and Bax, were explored with a yeast ***two*** - -*-hybrid*** system. Fusion proteins were created by linking Bcl-2 fam.ly proteins to a LexA DNA-binding domain or a B42 trans-activation demain. ***Proteir*** - ***protein*** ***interactions*** examined by expression of these fusion proteins in Saccharomyces cerevisiae having a lacZ (.beta.-galactosidase) gene under control of a. . . operator. This approach gave evidence for Bol-2 protein homodymerization. Bc1-2 also interacted with Bc1-X-L and Mc1-1 and with the dominant ***inhibitors*** Bax and Bol-X-S. Bol-X-L displayed the same pattern of combinatorial interactions with Bcl-2 family proteins as Bal- 2. Use of. . . Medical Descriptors: *protein family ****protein protein interaction*** article deletion mutant dimerization dna sequence enzyme assay numar. numan cell immumoblotting molecular cloning nonnuman phenotype plasmid polymerase chain reaction read the land saccharamyres derevisiae أأحب فيبار tnykruli protešti beta galactesidase cell extract complementary dna rna directed dna polymorase AMORRE OF SECRETARIES OF FRECHED SECRETARIES OF FRECHED SECRETARIES.

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Identification and comparison of ***protein*** - ***protein***
 ***interactions*** and identification of ***inhibitors***
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Methods are described for detecting ***protein*** - ***protein*** ***interactions*** , among two populations of proteins, each having a
complexity of at least 1,000. For example, proteins are fused either to.
. . and carrying one type each of the fusion proteins are mated
together. Productive interactions between the two halves due to
  ***protein*** - ***protein*** /**interactions*** lead to the
reconstitution of the transcriptional activator, which in turn leads to
the activation of a reporter gene contg.. . . carried out for two or
more populations of proteins. The differences in the genes encoding the
proteins involved in the ***protein*** - ***protein***

***interactions*** are characterized, thus leading to the identification
of specific ***protein*** - ***protein*** ***interactions***
and the genes encoding the interacting proteins, relevant to a particular
tissue, stage or disease. Furthermore, ***inhibitors*** that interfere with these ***protein*** - ***protein***
  ***interactions*** are identified by their ability to inactivate a
reporter gene. The screening for such ***inhibitors*** can be in a
multiplexed format where a set of ***inhibitors*** will be screened
against a library of interactors. Further, information-processing methods
and systems are described. These methods and systems provide for lawning at law or the sense of aims for detected interacting provide for account in a continuous sense of the continuous law of the continuous sense.
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       interaction between R4 and FKPF12; identification and comparison of
       identification of ""inhibitors"" )
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                           identification of ***inhibitors*** )
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                 unclassified); BIOL (Biological study); USES (Uses)
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                           ***protein*** - ***protein*** ***interactions*** and
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cDNA library
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     ***inhibitors***
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     (transcriptional regulatory domain, fusion proteins contg.;
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127464-60-2, Vascular endothelial growth factor
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            ANSWER 31 OF 33 CAPLUS COPYRIGHT 2000 ACS
***Two*** - ***hybrid*** screening and the cell cycle
             Yeast Two-Hybrid Syst. ( ***1997*** ), 133-196. Editor(s): Bartel, Paul
             L.; Fields, Stanley. Publisher: Oxford University Press, New York, N. Y.
             CODEN: 65YDA2
             A review with 61 refs. The ***two*** - ***hybrid*** screen has been
AB
             most often successful in the identification of stable, ***protein*** -
                  interactions are prevalent among components of cell cycle control, cell
              cycle regulatory proteins have proven amenable to the ***two*** -
                  ***hybrid*** approach. Here, the authors discusses three aspects of
              cell cycle control in which the ***two*** - ***hybrid*** technique
             has been of particular importance. These are the regulation of the G1/S
              transition by phosphorylation of pRb, global control of cell cycle
              progression by the p21/p27 family of cyclin-dependent kinase (CDK)
                   * frinhibitors ** and the role of CDK-activating kinase (CAK) and KAI in
              the metab. of threenine ~160 phosphorylation. ...tweeth of this bridge soreen call syste review
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                 inv.lvea in seel water
           1428.5-58-1, Cyclin-dependent kinase-activating kinase
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                  ***interactions*** involved in
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           150428-23-1, Cyclin-dependent kinase
          RL: BAC (Biological activity or effector, except adverse); BFR (Biological
          process); BIOL (Biological study); PROC (Process) (role of ***two*** - ***nybrid*** screening in analyzing
                 ***protein*** - ***protein***
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        ANSWER 33 OF 33 BIOSIS COPYRIGHT 2000 BIOSIS
          Biochemical and Biophysical Research Communications, (1995) Vol. 215, No.
           2, pp. 731-790.
           ISSN: 0006-291X.
          . . by its autoinhibitory domain (AID) and by the calcium-binding
AB.
           proteins calcineurin B (Cn5) and calmodulin. We have used the yeast
               ***twg*** - ***hybrid*** system to show that AID, CnB and calmoduling
           can only bind to a truncated catalytic subunit of yeast calcineurin [i.e.,. . . the mechanism by which drug-receptor complexes could
           modulate calcineurin activity but also unveil the possibility of
           identifying novel immunophilin-independent calcineurin ***inhibitors***
          which may disturb the association of ChAl-DELTA to AID.
          Miscellaneous Descriptors
CALCINEURIN B; CALMODULIN; DRUG-RECEPTOR COMPLEX; PHARMACODYNAMICS;
***PROTEIN*** - ***PROTEIN*** ***INTERACTION*** ; T-CELL
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